

#2

OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/912,157

DATE: 08/01/2001

TIME: 15:18:07

Input Set : A:\00-49.SEQ.txt

Output Set: N:\CRF3\08012001\I912157.raw

PS

4 <110> APPLICANT: Presnell, Scott R.
5 Kuestner, Rolf E.
6 Gao, Zeren
8 <120> TITLE OF INVENTION: Human Cytokine Receptor
10 <130> FILE REFERENCE: 00-49
C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/912,157
C--> 12 <141> CURRENT FILING DATE: 2001-07-23

ENTERED

12 <160> NUMBER OF SEQ ID NOS: 13
14 <170> SOFTWARE: FastSEQ for Windows Version 3.0
16 <210> SEQ ID NO: 1
17 <211> LENGTH: 2383
18 <212> TYPE: DNA
19 <213> ORGANISM: Homo sapiens
21 <220> FEATURE:
22 <221> NAME/KEY: CDS
23 <222> LOCATION: (86)...(2344)
25 <400> SEQUENCE: 1
26 ccgcgcgcgc caccgcccac tcggggctgg ccagcggcgg gcggccgggg cgacagagaac 60
27 ggccctggctg ggcgagcgca cggcc atg gcc ccg tgg ctg cag ctc tgc tcc 112
28 Met Ala Pro Trp Leu Gln Leu Cys Ser
29 1 5
31 gtc ttc ttt acg gtc aac gcc tgc ctc aac ggc tcg cag ctg gct gtg 160
32 Val Phe Phe Thr Val Asn Ala Cys Leu Asn Gly Ser Gln Leu Ala Val
33 10 15 20 25
35 gcc gct ggc ggg tcc ggc cgc gcg cgg gcc gcc gac acc tgt ggc tgg 208
36 Ala Ala Gly Gly Ser Gly Arg Ala Arg Gly Ala Asp Thr Cys Gly Trp
37 30 35 40
39 agg atg aaa gcg gct gcc cga ccc cgg ctt tgt gtt gct aat gag gga 256
40 Arg Met Lys Ala Ala Ala Arg Pro Arg Leu Cys Val Ala Asn Glu Gly
41 45 50 55
43 gtg ggg cca gcc agc aga aac agt ggg ctg tac aac atc acc ttc aaa 304
44 Val Gly Pro Ala Ser Arg Asn Ser Gly Leu Tyr Asn Ile Thr Phe Lys
45 60 65 70
47 tat gac aat tgt acc acc tac ttg aat cca gtg ggg aag cat gtg att 352
48 Tyr Asp Asn Cys Thr Thr Tyr Leu Asn Pro Val Gly Lys His Val Ile
49 75 80 85
51 gct gac gcc cag aat atc acc atc agc cag tat gct tgc cat gac caa 400
52 Ala Asp Ala Gln Asn Ile Thr Ile Ser Gln Tyr Ala Cys His Asp Gln
53 90 95 100 105
55 gtg gca gtc acc att ctt tgg tcc cca ggg gcc ctc ggc atc gaa ttc 448
56 Val Ala Val Thr Ile Leu Trp Ser Pro Gly Ala Leu Gly Ile Glu Phe
57 110 115 120
59 ctg aaa gga ttt cgg gta ata ctg gag gag ctg aag tcg gag gga aga 496
60 Leu Lys Gly Phe Arg Val Ile Leu Glu Glu Leu Lys Ser Glu Gly Arg
61 125 130 135
63 cag tgc caa caa ctg att cta aag gat ccg aag cag ctc aac agt agc 544
64 Gln Cys Gln Gln Leu Ile Leu Lys Asp Pro Lys Gln Leu Asn Ser Ser

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65	140	145	150	
67	ttc aaa aga act gga atg gaa tct caa cct ttc ctg aat atg aaa ttt	592		
68	Phe Lys Arg Thr Gly Met Glu Ser Gln Pro Phe Leu Asn Met Lys Phe			
69	155 160 165			
71	gaa acg gat tat ttc gta aag gtt gtc cct ttt cct tcc att aaa aac	640		
72	Glu Thr Asp Tyr Phe Val Lys Val Val Pro Phe Pro Ser Ile Lys Asn			
73	170 175 180 185			
75	gaa agc aat tac cac cct ttc ttc ttt aga acc cga gcc tgt gac ctg	688		
76	Glu Ser Asn Tyr His Pro Phe Phe Phe Arg Thr Arg Ala Cys Asp Leu			
77	190 195 200			
79	ttg tta cag ccg gac aat cta gct tgt aaa ccc ttc tgg aag cct cgg	736		
80	Leu Leu Gln Pro Asp Asn Leu Ala Cys Lys Pro Phe Trp Lys Pro Arg			
81	205 210 215			
83	aac ctg aac atc agc cag cat ggc tgc gac atg cag gtg tcc ttc gac	784		
84	Asn Leu Asn Ile Ser Gln His Gly Ser Asp Met Gln Val Ser Phe Asp			
85	220 225 230			
87	cat gca ccg cac aac ttc ggc ttc cgt ttc ttc tat ctt cac tac aag	832		
88	His Ala Pro His Asn Phe Gly Phe Arg Phe Phe Tyr Leu His Tyr Lys			
89	235 240 245			
91	ctc aag cac gaa gga cct ttc aag cga aag acc tgt aag cag gag caa	880		
92	Leu Lys His Glu Gly Pro Phe Lys Arg Lys Thr Cys Lys Gln Glu Gln			
93	250 255 260 265			
95	act aca gag acg acc agc tgc ctc ctt caa aat gtt tct cca ggg gat	928		
96	Thr Thr Glu Thr Thr Ser Cys Leu Leu Gln Asn Val Ser Pro Gly Asp			
97	270 275 280			
99	tat ata att gag ctg gtg gat gac act aac aca aca aga aaa gtg atg	976		
100	Tyr Ile Ile Glu Leu Val Asp Asp Thr Asn Thr Thr Arg Lys Val Met			
101	285 290 295			
103	cat tat gcc tta aag cca gtg cac tcc ccg tgg gcc ggg ccc atc aga	1024		
104	His Tyr Ala Leu Lys Pro Val His Ser Pro Trp Ala Gly Pro Ile Arg			
105	300 305 310			
107	gcc gtg gcc atc aca gtg cca ctg gta gtc ata tgc gca ttc gcg acg	1072		
108	Ala Val Ala Ile Thr Val Pro Leu Val Val Ile Ser Ala Phe Ala Thr			
109	315 320 325			
111	ctc ttc act gtg atg tgc cgc aag aag caa caa gaa aat ata tat tca	1120		
112	Leu Phe Thr Val Met Cys Arg Lys Lys Gln Gln Glu Asn Ile Tyr Ser			
113	330 335 340 345			
115	cat tta gat gaa gag agc tct gag tct tcc aca tac act gca gca ctc	1168		
116	His Leu Asp Glu Glu Ser Ser Glu Ser Ser Thr Tyr Thr Ala Ala Leu			
117	350 355 360			
119	cca aga gag agg ctc cgg ccg cgg ccg aag gtc ttt ctc tgc tat tcc	1216		
120	Pro Arg Glu Arg Leu Arg Pro Arg Pro Lys Val Phe Leu Cys Tyr Ser			
121	365 370 375			
123	agt aaa gat ggc cag aat cac atg aat gtc gtc cag tgt ttc gcc tac	1264		
124	Ser Lys Asp Gly Gln Asn His Met Asn Val Val Gln Cys Phe Ala Tyr			
125	380 385 390			
127	ttc ctc cag gac ttc tgt ggc tgt gag gtg gct ctg gac ctg tgg gaa	1312		
128	Phe Leu Gln Asp Phe Cys Gly Cys Glu Val Ala Leu Asp Leu Trp Glu			
129	395 400 405			

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131	gac ttc agc ctc tgt aga gaa ggg cag aga gaa tgg gtc atc cag aag	1360
132	Asp Phe Ser Leu Cys Arg Glu Gly Gln Arg Glu Trp Val Ile Gln Lys	
133	410 415 420 425	
135	atc cac gag tcc cag ttc atc att gtg gtt tgt tcc aaa ggt atg aag	1408
136	Ile His Glu Ser Gln Phe Ile Ile Val Val Cys Ser Lys Gly Met Lys	
137	430 435 440	
139	tac ttt gtg gac aag aag aac tac aaa cac aaa gga ggt ggc cga ggc	1456
140	Tyr Phe Val Asp Lys Lys Asn Tyr Lys His Lys Gly Gly Arg Gly	
141	445 450 455	
143	tcg ggg aaa gga gag ctc ttc ctg gtg gcg gtg tca gcc att gcc gaa	1504
144	Ser Gly Lys Gly Glu Leu Phe Leu Val Ala Val Ser Ala Ile Ala Glu	
145	460 465 470	
147	aag ctc cgc cag gcc aag cag agt tcg tcc gcg gcg ctc agc aag ttt	1552
148	Lys Leu Arg Gln Ala Lys Gln Ser Ser Ser Ala Ala Leu Ser Lys Phe	
149	475 480 485	
151	atc gcc gtc tac ttt gat tat tcc tgc gag gga gac gtc ccc ggt atc	1600
152	Ile Ala Val Tyr Phe Asp Tyr Ser Cys Glu Gly Asp Val Pro Gly Ile	
153	490 495 500 505	
155	cta gac ctg agt acc aag tac aga ctc atg gac aat ctt cct cag ctc	1648
156	Leu Asp Leu Ser Thr Lys Tyr Arg Leu Met Asp Asn Leu Pro Gln Leu	
157	510 515 520	
159	tgt tcc cac ttg cac tcc cga gac cac ggc ctc cag gag ccg ggg cag	1696
160	Cys Ser His Leu His Ser Arg Asp His Gly Leu Gln Glu Pro Gly Gln	
161	525 530 535	
163	cac acg cga cag ggc agc aga agg aac tac ttc cgg agc aag tca ggc	1744
164	His Thr Arg Gln Gly Ser Arg Arg Asn Tyr Phe Arg Ser Lys Ser Gly	
165	540 545 550	
167	cgg tcc cta tac gtc gcc att tgc aac atg cac cag ttt att gac gag	1792
168	Arg Ser Leu Tyr Val Ala Ile Cys Asn Met His Gln Phe Ile Asp Glu	
169	555 560 565	
171	gag ccc gac tgg ttc gaa aag cag ttc gtt ccc ttc cat cct cct cca	1840
174	Glu Pro Asp Trp Phe Gly Lys Gln Phe Val Pro Phe His Pro Pro Pro	
175	570 575 580 585	
177	ctg cgc tac cgg gag cca gtc ttg gag aaa ttt gat tcg ggc ttg gtt	1888
178	Leu Arg Tyr Arg Glu Pro Val Leu Glu Lys Phe Asp Ser Gly Leu Val	
179	590 595 600	
181	tta aat gat gtc atg tgc aaa cca ggg cct gag agt gac ttc tgc cta	1936
182	Leu Asn Asp Val Met Cys Lys Pro Gly Pro Glu Ser Asp Phe Cys Leu	
183	605 610 615	
185	aag gta gag gcg gct gtt ctt ggg gca acc gga cca gcc gac tcc cag	1984
186	Lys Val Glu Ala Ala Val Leu Gly Ala Thr Gly Pro Ala Asp Ser Gln	
187	620 625 630	
189	cac gag agt cag cat ggg ggc ctg gac caa gac ggg gag gcc cgg cct	2032
190	His Glu Ser Gln His Gly Gly Leu Asp Gln Asp Gly Glu Ala Arg Pro	
191	635 640 645	
193	gcc ctt gac ggt agc gcc gcc ctg caa ccc ctg ctg cac acg gtg aaa	2080
194	Ala Leu Asp Gly Ser Ala Ala Leu Gln Pro Leu Leu His Thr Val Lys	
195	650 655 660 665	
197	gcc ggc agc ccc tcg gac atg ccg cgg gac tca ggc atc tat gac tcg	2128

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198 Ala Gly Ser Pro Ser Asp Met Pro Arg Asp Ser Gly Ile Tyr Asp Ser
199          670          675          680
201 tct gtg ccc tca tcc gag ctg tct ctg cca ctg atg gaa gga ctc tcg      2176
202 Ser Val Pro Ser Ser Glu Leu Ser Leu Pro Leu Met Glu Gly Leu Ser
203          685          690          695
205 acg gac cag aca gaa acg tct tcc ctg acg gag agc gtg tcc tcc tct      2224
206 Thr Asp Gln Thr Glu Thr Ser Ser Leu Thr Glu Ser Val Ser Ser Ser
207          700          705          710
209 tca ggc ctg ggt gag gag gaa cct cct gcc ctt cct tcc aag ctc ctc      2272
210 Ser Gly Leu Gly Glu Glu Glu Pro Pro Ala Leu Pro Ser Lys Leu Leu
211          715          720          725
213 tct tct ggg tca tgc aaa gca gat ctt ggt tgc cgc agc tac act gat      2320
214 Ser Ser Gly Ser Cys Lys Ala Asp Leu Gly Cys Arg Ser Tyr Thr Asp
215 730          735          740          745
217 gaa ctc cac gcg gtc gcc cct ttg taacaaaacg aaagagtcta agcattgcc      2374
218 Glu Leu His Ala Val Ala Pro Leu
219          750
221 ctttagctg      2383
223 <210> SEQ ID NO: 2
224 <211> LENGTH: 753
225 <212> TYPE: PRT
226 <213> ORGANISM: Homo sapiens
228 <400> SEQUENCE: 2
229 Met Ala Pro Trp Leu Gln Leu Cys Ser Val Phe Phe Thr Val Asn Ala
230 1          5          10          15
231 Cys Leu Asn Gly Ser Gln Leu Ala Val Ala Ala Gly Gly Ser Gly Arg
232          20          25          30
233 Ala Arg Gly Ala Asp Thr Cys Gly Trp Arg Met Lys Ala Ala Ala Arg
234          35          40          45
235 Pro Arg Leu Cys Val Ala Asn Glu Gly Val Gly Pro Ala Ser Arg Asn
236          50          55          60
237 Ser Gly Leu Tyr Asn Ile Thr Phe Lys Tyr Asp Asn Cys Thr Thr Tyr
238 65          70          75          80
239 Leu Asn Pro Val Gly Lys His Val Ile Ala Asp Ala Gln Asn Ile Thr
240          85          90          95
241 Ile Ser Gln Tyr Ala Cys His Asp Gln Val Ala Val Thr Ile Leu Trp
242          100          105          110
243 Ser Pro Gly Ala Leu Gly Ile Glu Phe Leu Lys Gly Phe Arg Val Ile
244          115          120          125
245 Leu Glu Glu Leu Lys Ser Glu Gly Arg Gln Cys Gln Gln Leu Ile Leu
246          130          135          140
247 Lys Asp Pro Lys Gln Leu Asn Ser Ser Phe Lys Arg Thr Gly Met Glu
248 145          150          155          160
249 Ser Gln Pro Phe Leu Asn Met Lys Phe Glu Thr Asp Tyr Phe Val Lys
250          165          170          175
251 Val Val Pro Phe Pro Ser Ile Lys Asn Glu Ser Asn Tyr His Pro Phe
252          180          185          190
253 Phe Phe Arg Thr Arg Ala Cys Asp Leu Leu Leu Gln Pro Asp Asn Leu
254          195          200          205

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```

255 Ala Cys Lys Pro Phe Trp Lys Pro Arg Asn Leu Asn Ile Ser Gln His
256      210      215      220
257 Gly Ser Asp Met Gln Val Ser Phe Asp His Ala Pro His Asn Phe Gly
258 225      230      235      240
259 Phe Arg Phe Phe Tyr Leu His Tyr Lys Leu Lys His Glu Gly Pro Phe
260      245      250      255
261 Lys Arg Lys Thr Cys Lys Gln Glu Gln Thr Thr Glu Thr Thr Ser Cys
262      260      265      270
263 Leu Leu Gln Asn Val Ser Pro Gly Asp Tyr Ile Ile Glu Leu Val Asp
264      275      280      285
265 Asp Thr Asn Thr Thr Arg Lys Val Met His Tyr Ala Leu Lys Pro Val
266 290      295      300
267 His Ser Pro Trp Ala Gly Pro Ile Arg Ala Val Ala Ile Thr Val Pro
268 305      310      315      320
269 Leu Val Val Ile Ser Ala Phe Ala Thr Leu Phe Thr Val Met Cys Arg
270      325      330      335
271 Lys Lys Gln Gln Glu Asn Ile Tyr Ser His Leu Asp Glu Glu Ser Ser
272      340      345      350
273 Glu Ser Ser Thr Tyr Thr Ala Ala Leu Pro Arg Glu Arg Leu Arg Pro
274      355      360      365
275 Arg Pro Lys Val Phe Leu Cys Tyr Ser Ser Lys Asp Gly Gln Asn His
276 370      375      380
277 Met Asn Val Val Gln Cys Phe Ala Tyr Phe Leu Gln Asp Phe Cys Gly
278 385      390      395      400
279 Cys Glu Val Ala Leu Asp Leu Trp Glu Asp Phe Ser Leu Cys Arg Glu
280      405      410      415
281 Gly Gln Arg Glu Trp Val Ile Gln Lys Ile His Glu Ser Gln Phe Ile
282      420      425      430
283 Ile Val Val Cys Ser Lys Gly Met Lys Tyr Phe Val Asp Lys Lys Asn
284      435      440      445
285 Tyr Lys His Lys Gly Gly Gly Arg Gly Ser Gly Lys Gly Glu Leu Phe
286 450      455      460
287 Leu Val Ala Val Ser Ala Ile Ala Glu Lys Leu Arg Gln Ala Lys Gln
288 465      470      475      480
289 Ser Ser Ser Ala Ala Leu Ser Lys Phe Ile Ala Val Tyr Phe Asp Tyr
290      485      490      495
291 Ser Cys Glu Gly Asp Val Pro Gly Ile Leu Asp Leu Ser Thr Lys Tyr
292      500      505      510
293 Arg Leu Met Asp Asn Leu Pro Gln Leu Cys Ser His Leu His Ser Arg
294      515      520      525
295 Asp His Gly Leu Gln Glu Pro Gly Gln His Thr Arg Gln Gly Ser Arg
296 530      535      540
297 Arg Asn Tyr Phe Arg Ser Lys Ser Gly Arg Ser Leu Tyr Val Ala Ile
298 545      550      555      560
299 Cys Asn Met His Gln Phe Ile Asp Glu Glu Pro Asp Trp Phe Glu Lys
300      565      570      575
303 Gln Phe Val Pro Phe His Pro Pro Pro Leu Arg Tyr Arg Glu Pro Val
304      580      585      590
305 Leu Glu Lys Phe Asp Ser Gly Leu Val Leu Asn Asp Val Met Cys Lys

```

Use of n and/or Xaa has been detected in the Sequence Listing.
 Review the Sequence Listing to insure a corresponding
 explanation is presented in the <220> to <223> fields of
 each sequence using n or Xaa.

VERIFICATION SUMMARY

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Input Set : A:\00-49.SEQ.txt

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L:12 M:270 C: Current Application Number differs, Replaced Current Application No

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:341 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3

L:342 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3

L:343 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3

L:344 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3

L:345 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3

L:346 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3

L:347 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3

L:348 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3

L:349 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3

L:350 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3

L:351 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3

L:352 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3

L:353 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3

L:354 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3

L:355 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3

L:356 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3

L:357 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3

L:358 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3

L:359 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3

L:360 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3

L:361 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3

L:362 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3

L:363 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3

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L:376 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3

L:377 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3

L:378 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3

L:705 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6

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L:707 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6

L:708 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6

L:709 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6

L:710 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6

L:711 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6

L:712 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6

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L:713 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:714 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:715 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:716 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6